

ABSTRACT OF THE DISCLOSURE

The invention can be summarized as follows. There is provided a method for amplifying hypomethylated genomic nucleotide sequences and/or hypermethylated genomic nucleotide sequences and comparing the methylation state between different samples, for example control and test samples. Also disclosed is a microarray based method for analysing hypo and/or hypermethylated genomic nucleotide sequence. Further, kits comprising reagents for practising the method are provided.